

SEQUENCE LISTING

<110> Baum, Peter Robert
Fanslow III, William C.

<120> Molecules Designated LDCAM

<130> 2873-US

<140> to be assigned--

<141> 2001-02-06

<140> PCT/US99/17905

<141> 1999-08-05

<150> 60/095,672

<151> 1998-08-07

<160> 10

<170> PatentIn Ver. 2.0

<210> 1

<211> 1535

<212> DNA

<213> Homo sapien

<220> CDS

<221> 16..1341

<400> 1

```

gcgggccgcgc cgcac  atg gcg agt gta gtg ctg ccg agc gga tcc cag tgt  51
                Met Ala Ser Val Val Leu Pro Ser Gly Ser Gln Cys
                1                    5                10

gcg gcg gca gcg gcg gcg gcg gcg cct ccc ggg ctc cgg ctc cgg ctt  99
Ala Ala Ala Ala Ala Ala Ala Ala Pro Pro Gly Leu Arg Leu Arg Leu
                15                    20                25

ctg ctg ttg ctc ttc tcc gcc gcg gca ctg atc ccc aca ggt gat ggg  147
Leu Leu Leu Leu Phe Ser Ser Ala Ala Ala Leu Ile Pro Thr Gly Asp Gly
                30                    35                40

cag aat ctg ttt acg aaa gac gtg aca gtg atc gag gga gag gtt gcg  195
Gln Asn Leu Phe Thr Lys Asp Val Thr Val Ile Glu Gly Glu Val Ala
                45                    50                55                60

acc atc agt tgc caa gtc aat aag agt gac gac tct gtg att cag cta  243
Thr Ile Ser Cys Gln Val Asn Lys Ser Asp Asp Ser Val Ile Gln Leu
                65                    70                75

ctg aat ccc aac agg cag acc att tat ttc agg gac ttc agg cct ttg  291
Leu Asn Pro Asn Arg Gln Thr Ile Tyr Phe Arg Asp Phe Arg Pro Leu
                80                    85                90                95

aag gac agc agg ttt cag ttg ctg aat ttt tct agc agt gaa ctc aaa  339
Lys Asp Ser Arg Phe Gln Leu Leu Asn Phe Ser Ser Ser Glu Leu Lys
                95                    100                105

gta tca ttg aca aac gtc tca att tct gat gaa gga aga tac ttt tgc  387
Val Ser Leu Thr Asn Val Ser Ile Ser Asp Glu Gly Arg Tyr Phe Cys
                110                    115                120

```

cag ctc tat acc gat ccc cca cag gaa agt tac acc acc atc aca gtc	435
Gln Leu Tyr Thr Asp Pro Pro Gln Glu Ser Tyr Thr Thr Ile Thr Val	125 130 135 140
ctg gtc cca cca cgt aat ctg atg atc gat atc cag aaa gac act gcg	483
Leu Val Pro Pro Arg Asn Leu Met Ile Asp Ile Gln Lys Asp Thr Ala	145 150 155
gtg gaa ggt gag gag att gaa gtc aac tgc act gct atg gcc agc aag	531
Val Glu Gly Glu Glu Ile Glu Val Asn Cys Thr Ala Met Ala Ser Lys	160 165 170
cca gcc acg act atc agg tgg ttc aaa ggg aac aca gag cta aaa ggc	579
Pro Ala Thr Thr Ile Arg Trp Phe Lys Gly Asn Thr Glu Leu Lys Gly	175 180 185
aaa tcg gag gtg gaa gag tgg tca gac atg tac act gtg acc agt cag	627
Lys Ser Glu Val Glu Glu Trp Ser Asp Met Tyr Thr Val Thr Ser Gln	190 195 200
ctg atg ctg aag gtg cac aag gag gac gat ggg gtc cca gtg atc tgc	675
Leu Met Leu Lys Val His Lys Glu Asp Asp Gly Val Pro Val Ile Cys	205 210 215 220
cag gtg gag cac cct gcg gtc act gga aac ctg cag acc cag cgg tat	723
Gln Val Glu His Pro Ala Val Thr Gly Asn Leu Gln Thr Gln Arg Tyr	225 230 235
cta gaa gta cag tat aag cct caa gtg cac att cag atg act tat cct	771
Leu Glu Val Gln Tyr Lys Pro Gln Val His Ile Gln Met Thr Tyr Pro	240 245 250
cta caa ggc tta acc cgg gaa ggg gac gcg ctt gag tta aca tgt gaa	819
Leu Gln Gly Leu Thr Arg Glu Gly Asp Ala Leu Glu Leu Thr Cys Glu	255 260 265
gcc atc ggg aag ccc cag cct gtg atg gta act tgg gtg aga gtc gat	867
Ala Ile Gly Lys Pro Gln Pro Val Met Val Thr Trp Val Arg Val Asp	270 275 280
gat gaa atg cct caa cac gcc gta ctg tct ggg ccc aac ctg ttc atc	915
Asp Glu Met Pro Gln His Ala Val Leu Ser Gly Pro Asn Leu Phe Ile	285 290 295 300
aat aac cta aac aaa aca gat aat ggt aca tac cgc tgt gaa gct tca	963
Asn Asn Leu Asn Lys Thr Asp Asn Gly Thr Tyr Arg Cys Glu Ala Ser	305 310 315
aac ata gtg ggg aaa gct cac tcg gat tat atg ctg tat gta tac gat	1011
Asn Ile Val Gly Lys Ala His Ser Asp Tyr Met Leu Tyr Val Tyr Asp	320 325 330
ccc ccc aca act atc cct cct ccc aca acc acc acc acc acc acc	1059
Pro Thr Thr Thr Ile Pro Pro Thr Thr Thr Thr Thr Thr Thr Thr	335 340 345
acc acc acc acc acc atc ctt acc atc atc aca gat tcc cga gca ggt	1107
Thr Thr Thr Thr Thr Ile Leu Thr Thr Thr Thr Thr Thr Thr Thr	350 355 360
gaa gaa ggc tcg atc agg gca gtg gat cat gcc gtg atc ggt ggc gtc	1155
Glu Glu Gly Ser Ile Arg Ala Val Asp His Ala Val Ile Gly Gly Val	365 370 375 380
gtg gcg gtg gtg gtg ttc gcc atg ctg tgc ttg ctc atc att ctg ggg	1203
Val Ala Val Val Val Phe Ala Met Leu Cys Leu Leu Ile Ile Leu Gly	385 390 395

cgc tat ttt gcc aga cat aaa ggt aca tac ttc act cat gaa gcc aaa 1251
 Arg Tyr Phe Ala Arg His Lys Gly Thr Tyr Phe Thr His Glu Ala Lys
 400 405 410

gga gcc gat gac gca gca gac gca gac aca gct ata atc aat gca gaa 1299
 Gly Ala Asp Asp Ala Ala Asp Ala Asp Thr Ala Ile Ile Asn Ala Glu
 415 420 425

gga gga cag aac aac tcc gaa gaa aag aaa gag tac ttc atc 1341
 Gly Gly Gln Asn Asn Ser Glu Glu Lys Lys Glu Tyr Phe Ile
 430 435 440

tagatcagcc tttttgtttc aatgaggtgt ccaactggcc ctatttagat gataaagaga 1401
 cagtgtatatt ggaacttcgc agaaattcgt gtgttttttt atgaatgggt ggaaaggtgt 1461
 gagactggga aggcttgga tttgctgtgt aaaaaaaaa aaaaaatggt ctttgaaaag 1521
 aaaaaagcgg ccgctttctt attctatttc aacattcagc ttaatcataa tctctaaatc 1581
 atacatgcta tttccat 1598

<210> 2
 <211> 442
 <212> PRT
 <213> Homo sapien

<400> 2

Met Ala Ser Val Val Leu Pro Ser Gly Ser Gln Cys Ala Ala Ala Ala
 1 5 10 15

Ala Ala Ala Ala Pro Pro Gly Leu Arg Leu Arg Leu Leu Leu Leu
 20 25 30

Phe Ser Ala Ala Ala Leu Ile Pro Thr Gly Asp Gly Gln Asn Leu Phe
 35 40 45

Thr Lys Asp Val Thr Val Ile Glu Gly Glu Val Ala Thr Ile Ser Cys
 50 55 60

Gln Val Asn Lys Ser Asp Asp Ser Val Ile Gln Leu Leu Asn Pro Asn
 65 70 75 80

Arg Gln Thr Ile Tyr Phe Arg Asp Phe Arg Pro Leu Lys Asp Ser Arg
 85 90 95

Phe Gln Leu Leu Asn Phe Ser Ser Ser Glu Leu Lys Val Ser Leu Thr
 100 105 110

Asn Val Ser Ile Ser Asp Glu Gly Arg Tyr Phe Cys Gln Leu Tyr Thr
 115 120 125

Asp Pro Pro Gln Glu Ser Tyr Thr Thr Ile Thr Val Leu Val Pro Pro
 130 135 140

Arg Asn Leu Met Ile Asp Ile Gln Lys Asp Thr Ala Val Glu Gly Glu
 145 150 155 160

Glu Ile Glu Val Asn Cys Thr Ala Met Ala Ser Lys Pro Ala Thr Thr
 165 170 175

Ile Arg Trp Phe Lys Gly Asn Thr Glu Leu Lys Gly Lys Ser Glu Val
 180 185 190

Glu Glu Trp Ser Asp Met Tyr Thr Val Thr Ser Gln Leu Met Leu Lys
 195 200 205
 Val His Lys Glu Asp Asp Gly Val Pro Val Ile Cys Gln Val Glu His
 210 215 220
 Pro Ala Val Thr Gly Asn Leu Gln Thr Gln Arg Tyr Leu Glu Val Gln
 225 230 235 240
 Tyr Lys Pro Gln Val His Ile Gln Met Thr Tyr Pro Leu Gln Gly Leu
 245 250 255
 Thr Arg Glu Gly Asp Ala Leu Glu Leu Thr Cys Glu Ala Ile Gly Lys
 260 265 270
 Pro Gln Pro Val Met Val Thr Trp Val Arg Val Asp Asp Glu Met Pro
 275 280 285
 Gln His Ala Val Leu Ser Gly Pro Asn Leu Phe Ile Asn Asn Leu Asn
 290 295 300
 Lys Thr Asp Asn Gly Thr Tyr Arg Cys Glu Ala Ser Asn Ile Val Gly
 305 310 315 320
 Lys Ala His Ser Asp Tyr Met Leu Tyr Val Tyr Asp Pro Pro Thr Thr
 325 330 335
 Ile Pro Pro Pro Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr
 340 345 350
 Thr Ile Leu Thr Ile Ile Thr Asp Ser Arg Ala Gly Glu Glu Gly Ser
 355 360 365
 Ile Arg Ala Val Asp His Ala Val Ile Gly Gly Val Val Ala Val Val
 370 375 380
 Val Phe Ala Met Leu Cys Leu Leu Ile Ile Leu Gly Arg Tyr Phe Ala
 385 390 395 400
 Arg His Lys Gly Thr Tyr Phe Thr His Glu Ala Lys Gly Ala Asp Asp
 405 410 415
 Ala Ala Asp Ala Asp Thr Ala Ile Ile Asn Ala Glu Gly Gly Gln Asn
 420 425 430
 Asn Ser Glu Glu Lys Lys Glu Tyr Phe Ile
 435 440

<210> 3
 <211> 1935
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> 2..1272

<400> 3

g g c g c g c c c c a g g g c t c c g g c t c c g g c t c c t g c t g t t g c t c c t t 46
 Ala Ala Pro Pro Gly Leu Arg Leu Arg Leu Leu Leu Leu Leu 15
 1 5 10
 t c g g c c g c g c a c t g a t c c c a c a g g t g a t g g a c a g a a t c t g t t t a c t 94
 Ser Ala Ala Ala Leu Ile Pro Thr Gly Asp Gly Gln Asn Leu Phe Thr

Thr Asp Asn Gly Thr Tyr Arg Cys Glu Ala Ser Asn Ile Val Gly Lys
 290 295 300
 gct cat tcg gac tat atg ctg tat gta tac gat ccc ccc aca act atc 958
 Ala His Ser Asp Tyr Met Leu Tyr Val Tyr Asp Pro Pro Thr Thr Ile
 305 310 315
 cct cct ccc aca aca acc acc acc act acc acc acc acc acc acc 1006
 Pro Pro Pro Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr
 320 325 330 335
 atc ctt acc atc atc aca gat tct cga gca ggt gaa gag ggg acc att 1054
 Ile Leu Thr Ile Ile Thr Asp Ser Arg Ala Gly Glu Glu Gly Thr Thr
 340 345 350
 ggg gca gtg gac cac gca gtg att ggt ggc gtc gta gcc gtg gtg gtg 1102
 Gly Ala Val Asp His Ala Val Ile Gly Gly Val Ala Val Val Val Val
 355 360 365
 ttt gcc atg cta tgc ttg ctc atc att ctg ggc cgc tat ttt gcc aga 1150
 Phe Ala Met Leu Cys Leu Leu Ile Ile Leu Gly Arg Tyr Phe Ala Arg
 370 375 380
 cat aaa ggt aca tac ttc act cat gaa gcc aaa gga gcc gat gac gca 1198
 His Lys Gly Thr Tyr Phe Thr His Glu Ala Lys Gly Ala Asp Asp Ala
 385 390 395
 gca gac gca gac aca gct ata atc aat gca gaa gga gga cag aac aac 1246
 Ala Asp Ala Asp Thr Ala Ile Ile Asn Ala Glu Gly Gly Gln Asn Asn
 400 405 410 415
 tcc gaa gaa aag aaa gag tac ttc at ctatgcagc ctttttgttc 1292
 Ser Glu Glu Lys Lys Glu Tyr Phe
 420
 caatgagggtg tccaactggc ctgttttagat gataaagaga cagtgtactt ggaactttcg 1352
 agaagctcgt gtggtttttt gttttgtttt gtttttttat gagtgggtgg agagatgcga 1412
 gactgggaag gcttgggatt tgcaatgtac aaacaaaaac aaagaatgtt ctttgaagt 1472
 acactctgct gtttgacacc tctttttaat ctggttttta tttgctttgg gttttgggtt 1532
 tttttgggtt tttgtttttt tcatttatat ttcttctac caagtcaaac ttgggtactt 1592
 ggatttgggtt tcggttagatt gcagaaaatt ctgtgccttg tttttcattc gtttgtgtg 1652
 tttcttccct ctgtgccatt tatttttccc aaaatcaaat ttgttttttt cccctccca 1712
 aacctcccat tttttggaat tgacctgctg gaattcttaa gactttctcc ctgttgccag 1772
 tttcttttat ttgtgttaac ggtgactgct ttctgttcca aattcagttt cataaaagga 1832
 aaaccagcac aatttagatt tcatagtcca gaatttagtg tctccatgat gcacctttct 1892
 ctgtgtgtgt aaagatttgg gtgaagaaaa aaaaaaaaaa aaa 1935

 <210> 4
 <211> 423
 <212> PRT
 <213> Mus musculus

 <400> 4
 Ala Ala Pro Pro Gly Leu Arg Leu Arg Leu Leu Leu Leu Leu Ser

1	5	10	15
Ala Ala Ala Leu Ile Pro Thr Gly Asp Gly Gln Asn Leu Phe Thr Lys	20	25	30
Asp Val Thr Val Ile Glu Gly Glu Val Ala Thr Ile Ser Cys Gln Val	35	40	45
Asn Lys Ser Asp Asp Ser Val Ile Gln Leu Leu Asn Pro Asn Arg Gln	50	55	60
Thr Ile Tyr Phe Arg Asp Phe Arg Pro Leu Lys Asp Ser Arg Phe Gln	65	70	75
Leu Leu Asn Phe Ser Ser Ser Glu Leu Lys Val Ser Leu Thr Asn Val	85	90	95
Ser Ile Ser Asp Glu Gly Arg Tyr Phe Cys Gln Leu Tyr Thr Asp Pro	100	105	110
Pro Gln Glu Ser Tyr Thr Thr Ile Thr Val Leu Val Pro Pro Arg Asn	115	120	125
Leu Met Ile Asp Ile Gln Lys Asp Thr Ala Val Glu Gly Glu Ile	130	135	140
Glu Val Asn Cys Thr Ala Met Ala Ser Lys Pro Ala Thr Thr Ile Arg	145	150	155
Trp Phe Lys Gly Asn Lys Glu Leu Lys Gly Lys Ser Glu Val Glu Glu	165	170	175
Trp Ser Asp Met Tyr Thr Val Thr Ser Gln Leu Met Leu Lys Val His	180	185	190
Lys Glu Asp Asp Gly Val Pro Val Ile Cys Gln Val Glu His Pro Ala	195	200	205
Val Thr Gly Asn Leu Gln Thr Gln Arg Tyr Leu Glu Val Gln Tyr Lys	210	215	220
Pro Gln Val His Ile Gln Met Thr Tyr Pro Leu Gln Gly Leu Thr Arg	225	230	235
Glu Gly Asp Ala Phe Glu Leu Thr Cys Glu Ala Ile Gly Lys Pro Gln	245	250	255
Pro Val Met Val Thr Trp Val Arg Val Asp Asp Glu Met Pro Gln His	260	265	270
Ala Val Leu Ser Gly Pro Asn Leu Phe Ile Asn Asn Leu Asn Lys Thr	275	280	285
Asp Asn Gly Thr Tyr Arg Cys Glu Ala Ser Asn Ile Val Gly Lys Ala	290	295	300
His Ser Asp Tyr Met Leu Tyr Val Tyr Asp Pro Pro Thr Thr Ile Pro	305	310	315
Pro Pro Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Ile	325	330	335
Leu Thr Ile Ile Thr Asp Ser Arg Ala Gly Glu Glu Gly Thr Ile Gly	340	345	350
Ala Val Asp His Ala Val Ile Gly Gly Val Val Ala Val Val Val Phe	355	360	365

Ala Met Leu Cys Leu Leu Ile Ile Leu Gly Arg Tyr Phe Ala Arg His
370 375 380

Lys Gly Thr Tyr Phe Thr His Glu Ala Lys Gly Ala Asp Asp Ala Ala
385 390 395 400

Asp Ala Asp Thr Ala Ile Ile Asn Ala Glu Gly Gly Gln Asn Asn Ser
405 410 415

Glu Glu Lys Lys Glu Tyr Phe
420

<210> 5
<211> 29
<212> Oligonucleotide
<213> Homo sapien

<400> 5
tatgtcgaca tggcgagtgt agtgctgcc 29

<210> 6
<211> 30
<212> Oligonucleotide
<213> Homo sapien

<400> 6
atatagatct atgatccact gccctgatcg 30

<210> 7
<211> 1820
<212> DNA
<213> Homo sapien

<220> CDS
<221> 157..1452
<222>

<400> 7
aagcttgcca cgaggcggtc cccacctcgg ccccgggctc cgaagcggct cgggggcgcc 60
ctttcggtca acatcgtagt ccacccctc cccatcccca gcccccggg attcaggctc 120
gccagcgccc agccaggag cggccggga agcgcg atg ggg gcc cca gcc gcc 174
Met Gly Ala Pro Ala Ala
1 5
tcg ctc ctg ctc ctg ctc ctg ctg ttc gcc tgc tgc tgg gcg ccc ggc 222
Ser Leu Leu Leu Leu Leu Leu Leu Phe Ala Cys Cys Trp Ala Pro Gly
10 15 20
ggg gcc aac ctc tcc cag gac gcc tac tgg cag gag cag gat ttg gag 270
Gly Ala Asn Leu Ser Gln Asp Gly Tyr Trp Gln Glu Gln Asp Leu Glu
25 30 35
ctg gga act ctg gct cca ctc gac gag gcc atc agc tcc aca gtc tgg 318
Leu Gly Thr Leu Ala Pro Leu Asp Glu Ala Ile Ser Ser Thr Val Trp
40 45 50
agc agc cct gac atg ctg gcc agt caa gac agc cag ccc tgg aca tct 366
Ser Ser Pro Asp Met Leu Ala Ser Gln Asp Ser Gln Pro Trp Thr Ser

55	60	65	70	
gat gaa aca gtg gtg gct ggt ggc acc gtg gtg ctc aag tgc caa gtg	75	80		414
Asp Glu Thr Val Val Ala Gly Gly Thr Val Val Leu Lys Cys Gln Val			85	
aaa gat cac gag gac tca tcc ctg caa tgg tct aac cct gct cag cag	90	95	100	462
Lys Asp His Tyr Asp Ser Ser Leu Gln Trp Ser Asn Pro Ala Gln Gln				
act ctc tac ttt ggg gag aag aga gcc ctt cga gat aat cga att cag	105	110	115	510
Thr Leu Tyr Phe Gly Glu Lys Arg Ala Leu Arg Asp Asn Arg Ile Gln				
ctg gtt acc tct acg ccc cac gag ctc agc atc agc atc agc aat gtg	120	125	130	558
Leu Val Thr Ser Thr Pro Glu Glu Leu Ser Ile Ser Ile Ser Asn Val				
gcc ctg gca gac gag ggc gag tac acc tgc tca atc ttc act atg cct	135	140	145	606
Ala Leu Ala Asp Glu Gly Glu Tyr Thr Cys Ser Ile Phe Thr Met Pro			150	
gtg cga act gcc aag tcc ctc gtc act gtg cta gga att cca cag aag	155	160	165	654
Val Arg Thr Ala Lys Ser Leu Val Thr Val Leu Gly Ile Pro Gln Lys				
ccc atc atc act ggt tat aaa tct tca tta cgg gaa aaa gac aca gcc	170	175	180	702
Pro Ile Ile Thr Gly Tyr Lys Ser Ser Leu Arg Glu Lys Asp Thr Ala				
acc cta aac tgt cag tct tct ggg agc aag cct gca gcc cgg ctc acc	185	190	195	750
Thr Leu Asn Cys Gln Ser Ser Gly Ser Lys Pro Ala Ala Arg Leu Thr				
tgg aga aag ggt gac caa gaa ctc cac gga gaa cca acc cgc ata cag	200	205	210	798
Trp Arg Lys Gly Asp Gln Glu Leu His Gly Glu Pro Thr Arg Ile Gln				
gaa gat ccc aat ggt aaa acc ttc act gtc agc agc tgc gtg aca ttc	215	220	225	846
Glu Asp Pro Asn Gly Lys Thr Phe Thr Val Ser Ser Ser Val Thr Phe			230	
cag gtt acc cgg gag gat gat ggg gcg agc atc gtg tgc tct gtg aac	235	240	245	894
Gln Val Thr Arg Glu Asp Asp Gly Ala Ser Ile Val Cys Ser Val Asn				
cat gaa tct cta aag gga gct gac aga tcc acc tct tct caa cgc att gaa	250	255	260	942
His Glu Ser Leu Lys Gly Ala Asp Arg Ser Ser Ser Arg Ile Gln				
gtt tta tac aca cca act gcg atg att agg cca gac cct ccc att cct	265	270	275	990
Val Leu Tyr Thr Pro Thr Ala Met Ile Arg Pro Asp Pro Pro His Pro				
cgt gag ggc cag aag ctg ttg cta cac tgt gag ggt cgc ggc aat cca	280	285	290	1038
Arg Glu Gly Gln Lys Leu Leu Leu His Cys Glu Gly Arg Gly Asn Pro				
gtc ccc cag cag tac cta tgg gag aag gag ggc agt gtg cca ccc ctg	295	300	305	1086
Val Pro Gln Gln Tyr Leu Trp Glu Lys Glu Gly Ser Val Pro Pro Leu			310	
aag atg acc cag gag agt gcc ctg atc ttc cct ttc ctc aac aag agt	315	320	325	1134
Lys Met Thr Gln Glu Ser Ala Leu Ile Phe Pro Phe Leu Asn Lys Ser				
gac agt ggc acc tac ggc tgc aca gcc acc agc aac atg ggc agc tac				1182

Asp Ser Gly Thr Tyr Gly Cys Thr Ala Thr Ser Asn Met Gly Ser Tyr
 330 335 340
 aag gcc tac tac acc ctc aat gtt aat gac ccc agt ccg gtg ccc tcc 1230
 Lys Ala Tyr Tyr Thr Leu Asn Val Asn Asp Pro Ser Pro Val Pro Ser
 345 350 355
 tcc tcc agc acc tac cac gcc atc atc ggt ggg atc gtg gct ttc att 1278
 Ser Ser Ser Thr Tyr His Ala Ile Ile Gly Gly Ile Val Ala Phe Ile
 360 365 370
 gtc ttc ctg ctg ctc atc atg ctc atc ttc ctt ggc cac tac ttg atc 1326
 Val Phe Leu Leu Leu Ile Met Leu Ile Phe Leu Gly His Tyr Leu Ile
 375 380 385 390
 cgg cac aaa gga acc tac ctg aca cat gag gca aaa ggc tcc gac gat 1374
 Arg His Lys Gly Thr Tyr Leu Thr His Glu Ala Lys Gly Ser Asp Asp
 395 400 405
 gct cca gac gcg gac acg gcc atc atc aat gca gaa ggc ggg cag tca 1422
 Ala Pro Asp Ala Asp Thr Ala Ile Ile Asn Ala Glu Gly Gly Phe Ser
 410 415 420
 gga ggg gac gac aag aag gaa tat ttc atc tagaggcgcc tgcccacttc 1472
 Gly Gly Asp Asp Lys Lys Glu Tyr Phe Ile
 425 430
 ctgcgcccc cagggggccct gtggggactg ctggggccgt caccaacccg gaactgtaca 1532
 gagcaacccg agggccgccc ctcccgttg ctccccagcc caccaccccc cctgtacaga 1592
 atgtctgctt tgggtgcggt ttgtactcg gtttgggaatg gggaggaggagg agggcggggg 1652
 gaggggaggg ttgccctcag ccctttccgt ggctctcttg catttgggtt attattattt 1712
 ttgtaacaat cccaaatcaa atctgtctcc aggcgtggaga ggcaggagcc ctgggggtgag 1772
 aaaagcaaaa aacaacaaaa aaaaaaaaaa aaaaattcct gcggccgc 1820

 <210> 8
 <211> 432
 <212> PRT
 <213> Homo sapien

 <400> 8
 Met Gly Ala Pro Ala Ala Ser Leu Leu Leu Leu Leu Leu Phe Ala
 1 5 10 15
 Cys Cys Trp Ala Pro Gly Gly Ala Asn Leu Ser Gln Asp Gly Tyr Trp
 20 25 30
 Gln Glu Gln Asp Leu Glu Leu Gly Thr Leu Ala Pro Leu Asp Glu Ala
 35 40 45
 Ile Ser Ser Thr Val Trp Ser Ser Pro Asp Met Leu Ala Ser Gln Asp
 50 55 60
 Ser Gln Pro Trp Thr Ser Asp Glu Thr Val Val Ala Gly Gly Thr Val
 65 70 75 80
 Val Leu Lys Cys Gln Val Lys Asp His Glu Asp Ser Ser Leu Gln Trp
 85 90 95
 Ser Asn Pro Ala Gln Gln Thr Leu Tyr Phe Gly Glu Lys Arg Ala Leu
 100 105 110

Arg Asp Asn Arg Ile Gln Leu Val Thr Ser Thr Pro His Glu Leu Ser
 115 120
 Ile Ser Ile Ser Asn Val Ala Leu Ala Asp Glu Gly Glu Tyr Thr Cys
 130 135 140
 Ser Ile Phe Thr Met Pro Val Arg Thr Ala Lys Ser Leu Val Thr Val
 145 150 155 160
 Leu Gly Ile Pro Gln Lys Pro Ile Ile Thr Gly Tyr Lys Ser Ser Leu
 165 170 175
 Arg Glu Lys Asp Thr Ala Thr Leu Asn Cys Gln Ser Ser Gly Ser Lys
 180 185 190
 Pro Ala Ala Arg Leu Thr Trp Arg Lys Gly Asp Gln Glu Leu His Gly
 195 200 205
 Glu Pro Thr Arg Ile Gln Glu Asp Pro Asn Gly Lys Thr Phe Thr Val
 210 215 220
 Ser Ser Ser Val Thr Phe Gln Val Thr Arg Glu Asp Asp Gly Ala Ser
 225 230 235 240
 Ile Val Cys Ser Val Asn His Glu Ser Leu Lys Gly Ala Asp Arg Ser
 245 250 255
 Thr Ser Gln Arg Ile Glu Val Leu Tyr Thr Pro Thr Ala Met Ile Arg
 260 265 270
 Pro Asp Pro Pro His Pro Arg Glu Gly Gln Lys Leu Leu Leu His Cys
 275 280 285
 Glu Gly Arg Gly Asn Pro Val Pro Gln Gln Tyr Leu Trp Glu Lys Glu
 290 295 300
 Gly Ser Val Pro Pro Leu Lys Met Thr Gln Glu Ser Ala Leu Ile Phe
 305 310 315 320
 Pro Phe Leu Asn Lys Ser Asp Ser Gly Thr Tyr Gly Cys Thr Ala Thr
 325 330 335
 Ser Asn Met Gly Ser Tyr Lys Ala Tyr Tyr Thr Leu Asn Val Asn Asp
 340 345 350
 Pro Ser Pro Val Pro Ser Ser Ser Ser Thr Tyr His Ala Ile Ile Gly
 355 360 365
 Gly Ile Val Ala Phe Ile Val Phe Leu Leu Leu Ile Met Leu Ile Phe
 370 375 380
 Leu Gly His Tyr Leu Ile Arg His Lys Gly Thr Tyr Leu Thr His Glu
 385 390 395 400
 Ala Lys Gly Ser Asp Asp Ala Pro Asp Ala Asp Thr Ala Ile Ile Asn
 405 410 415
 Ala Glu Gly Gly Gln Ser Gly Gly Asp Asp Lys Lys Glu Tyr Phe Ile
 420 425 430

<210> 9
 <211> 1718
 <212> DNA
 <213> Homo sapien

<220>
 <221> CDS
 <222> 157..1350
 <400> 9

aagcttgcca cgaggcggtc cccacctcgg ccccgggctc cgaagcggtc cgggggcgcc 60
 ctttcgtgcca acatcgtagt ccaacccctc cccatcccca gccccggggg attcaggctc 120
 gccagcgccc agccaggagg cgggcccggga agcgcg atg ggg gcc cca gcc gcc 174
 Met Gly Ala Pro Ala Ala
 1 5
 tgc ctc ctg ctc ctg ctc ctg etg ttc gcc tgc tgc tgg gcg ccc gcc 222
 Ser Leu Leu Leu Leu Leu Leu Phe Ala Cys Cys Trp Ala Pro Gly
 10 15 20
 ggg gcc aac ctc tcc cag gac gac agc cag ccc tgg aca tct gat gaa 270
 Gly Ala Asn Leu Ser Gln Asp Asp Ser Gln Pro Trp Thr Ser Asp Glu
 25 30 35
 aca gtg gtg gct ggt ggc acc gtg gtg ctc aag tgc caa gtg aaa gat 318
 Thr Val Val Ala Gly Gly Thr Val Val Leu Lys Cys Gln Val Lys Asp
 40 45 50
 cac gag gac tca tcc ctg caa tgg tct aac cct gct cag cag act ctc 366
 His Glu Asp Ser Ser Leu Gln Trp Ser Asn Pro Ala Gln Gln Thr Leu
 55 60 65 70
 tac ttt ggg gag aag aga gcc ctt cga gat aat cga att cag ctg gtt 414
 Tyr Phe Gly Glu Lys Arg Ala Leu Arg Asp Asn Arg Ile Gln Leu Val
 75 80 85
 acc tct acg ccc cac gag ctc agc atc agc atc agc aat gtg gcc ctg 462
 Thr Ser Thr Pro His Glu Leu Ser Ile Ser Ile Ser Asn Val Ala Leu
 90 95 100
 gca gac gag ggc gag tac acc tgc tca atc ttc act atg cct gtg cga 510
 Ala Asp Glu Gly Glu Tyr Thr Cys Ser Ile Phe Thr Met Pro Val Arg
 105 110 115
 act gcc aag tcc ctc gtc act gtg cta gga att cca cag aag ccc atc 558
 Thr Ala Lys Ser Leu Val Thr Val Leu Gly Ile Pro Gln Lys Pro Ile
 120 125 130
 atc act ggt tat aaa tct tca tta cgg gaa aaa gac aca gcc acc cta 606
 Ile Thr Gly Tyr Lys Ser Ser Leu Arg Glu Lys Asp Thr Ala Thr Leu
 135 140 145 150
 aac tgt cag tct tct ggg agc aag cct gca gcc cgg ctc acc tgg aga 654
 Asn Cys Glu Ser Ser Gly Ser Lys Pro Ala Ala Arg Leu Thr Trp Arg
 155 160 165
 aag ggt gac caa gaa ctc cac gga gaa cca acc cgc ata cag gaa gat 702
 Lys Gly Asp Gln Glu Leu His Gly Glu Pro Thr Arg Ile Gln Glu Asp
 170 175 180
 ccc aat ggt aaa acc ttc act gtc agc agc tgc gtg aca ttc cag gtt 750
 Pro Asn Gly Lys Thr Phe Thr Val Ser Ser Ser Val Thr Phe Gln Val
 185 190 195
 acc cgg gag gat gat ggg gcg agc atc gtg tgc tct gtg aac cat gaa 798
 Thr Arg Glu Asp Asp Gly Ala Ser Ile Val Cys Ser Val Asn His Glu
 200 205 210
 tct cta aag gga gct gac aga tcc acc tct caa cgc att gaa gtt tta 846

Ser Leu Lys Gly Ala Asp Arg Ser Thr Ser Gln Arg Ile Glu Val Leu
 215 220 225 230
 tac aca cca act gcg atg att agg cca gac cct ccc cat cct cgt gag 894
 Tyr Thr Pro Thr Ala Met Ile Arg Pro Asp Pro His Pro Arg Glu
 235 240 245
 ggc cag aag ctg ttg cta cac tgt gag ggt cgc ggc aat cca gtc ccc 942
 Gly Leu Lys Leu Leu His Cys Gly Arg Gly Asn Pro Val Pro
 250 255 260
 cag cag tac cta tgg gag aag gag ggc agt gtg cca ccc ctg aag atg 990
 Gln Gln Tyr Leu Trp Glu Lys Glu Gly Ser Val Pro Pro Leu Lys Met
 265 270 275
 acc cag gag agt gcc ctg atc ttc cct ttc ctc aac aag agt gac agt 1038
 Thr Gln Glu Ser Ala Leu Ile Phe Pro Phe Leu Asn Lys Ser Asp Ser
 280 285 290
 ggc acc tac gcc tgc aca gcc acc agc aac atg ggc agc tac aag gcc 1086
 Gly Thr Tyr Gly Cys Thr Ala Thr Ser Asn Met Gly Ser Tyr Lys Ala
 295 300 305
 tac tac acc ctc aat gtt aat gac ccc agt ccg gtg ccc tcc tcc tcc 1134
 Tyr Tyr Thr Leu Asn Val Asn Asp Pro Ser Pro Val Pro Ser Ser Ser
 315 320 325
 agc acc tac cac gcc atc atc ggt ggg atc gtg gct ttc att gtc ttc 1182
 Ser Thr Tyr His Ala Ile Ile Gly Gly Ile Val Ala Phe Ile Val Phe
 330 335 340
 ctg ctg ctc atc atg ctc atc ttc ctt ggc cac tac ttg atc cgg cac 1230
 Leu Leu Leu Ile Met Leu Ile Phe Leu Gly His Tyr Leu Ile Arg His
 345 350 355
 aaa gga acc tac ctg aca cat gag gca aaa ggc tcc gac gat gct cca 1278
 Lys Gly Thr Tyr Leu Thr His Glu Ala Lys Gly Ser Asp Asp Ala Pro
 360 365 370
 gac gcg gac acg gcc atc atc aat gca gaa ggc ggg cag tca gga ggg 1326
 Asp Ala Asp Thr Ala Ile Ile Asn Ala Glu Gly Gly Gln Ser Gly Gly
 375 380 385 390
 gac gac aag aag gaa tat ttc atc tagaggcgcc tgcccacttc ctgcgcccc 1380
 Asp Asp Lys Lys Glu Tyr Phe Ile
 395
 cagggggcct gtggggactg ctggggcggt caccaccccg gactgtgaca gagcaaccgc 1440
 agggccgccc ctcccgcttg cteccagccc caccaccccc cctgtacaga atgtctgctt 1500
 tgggtgcggt tttgtactcg gtttgaatg gggaggaggagg agggcggggg gaggggaggg 1560
 ttgcctcag ccttttcctg ggcttctctg catttggtt attattattt ttgtaacaat 1620
 cccaaatcaa atctgtctcc aggctggaga ggcaggagcc ctggggtgag aaaagcaaaa 1680
 aacaaacaaa aaaaaaaaaa aaaaattcct gcggcgcc 1718

 <210> 10
 <211> 398
 <212> PRT
 <213> Homo sapien

 <400> 10

Met Gly Ala Pro Ala Ala Ser Leu Leu Leu Leu Leu Leu Phe Ala
 1 5 10 15
 Cys Cys Trp Ala Pro Gly Gly Ala Asn Leu Ser Gln Asp Asp Ser Gln
 20 25 30
 Pro Trp Thr Ser Asp Glu Thr Val Val Ala Gly Gly Thr Val Val Leu
 35 40 45
 Lys Cys Gln Val Lys Asp His Glu Asp Ser Ser Leu Gln Trp Ser Asn
 50 55 60
 Pro Ala Gln Gln Thr Leu Tyr Phe Gly Glu Lys Arg Ala Leu Arg Asp
 65 70 75 80
 Asn Arg Ile Gln Leu Val Thr Ser Thr Pro His Glu Leu Ser Ile Ser
 85 90 95
 Ile Ser Asn Val Ala Leu Ala Asp Glu Gly Glu Tyr Thr Cys Ser Ile
 100 105 110
 Phe Thr Met Pro Val Arg Thr Ala Lys Ser Leu Val Thr Val Leu Gly
 115 120 125
 Ile Pro Gln Lys Pro Ile Ile Thr Gly Tyr Lys Ser Ser Leu Arg Glu
 130 135 140
 Lys Asp Thr Ala Thr Leu Asn Cys Gln Ser Ser Gly Ser Lys Pro Ala
 145 150 155 160
 Ala Arg Leu Thr Trp Arg Lys Gly Asp Gln Glu Leu His Gly Glu Pro
 165 170 175
 Thr Arg Ile Gln Glu Asp Pro Asn Gly Lys Thr Phe Thr Val Ser Ser
 180 185 190
 Ser Val Thr Phe Gln Val Thr Arg Glu Asp Asp Gly Ala Ser Ile Val
 195 200 205
 Cys Ser Val Asn His Glu Ser Leu Lys Gly Ala Asp Arg Ser Thr Ser
 210 215 220
 Gln Arg Ile Glu Val Leu Tyr Thr Pro Thr Ala Met Ile Arg Pro Asp
 225 230 235 240
 Pro Pro His Pro Arg Glu Gly Gln Lys Leu Leu Leu His Cys Glu Gly
 245 250 255
 Arg Gly Asn Pro Val Pro Gln Gln Tyr Leu Trp Glu Lys Glu Gly Ser
 260 265 270
 Val Pro Pro Leu Lys Met Thr Gln Glu Ser Ala Leu Ile Phe Pro Phe
 275 280 285
 Leu Asn Lys Ser Asp Ser Gly Thr Tyr Gly Cys Thr Ala Thr Ser Asn
 290 295 300
 Met Gly Ser Tyr Lys Ala Tyr Tyr Thr Leu Asn Val Asn Asp Pro Ser
 305 310 315 320
 Pro Val Pro Ser Ser Ser Thr Tyr His Ala Ile Ile Gly Gly Ile
 325 330 335
 Val Ala Phe Ile Val Phe Leu Leu Leu Ile Met Leu Ile Phe Leu Gly
 340 345 350
 His Tyr Leu Ile Arg His Lys Gly Thr Tyr Leu Thr His Glu Ala Lys

355						360						365			
Gly	Ser	Asp	Asp	Ala	Pro	Asp	Ala	Asp	Thr	Ala	Ile	Ile	Asn	Ala	Glu
	370					375					380				
Gly	Gly	Gln	Ser	Gly	Gly	Asp	Asp	Lys	Lys	Glu	Tyr	Phe	Ile		
385					390					395					